

# SCORE Search Results Details for Application 098833 and Search Result us-09-883-343a-19.rnpbm.

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This page gives you Search Results detail for the Application 09883343 and Search Result us-09-883-343a-19  
[start](#)

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GenCore version 5.1.7  
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OM nucleic - nucleic search, using sw model

Run on: May 3, 2006, 22:50:07 ; Search time 512 Seconds  
(without alignments)  
2745.692 Million cell updates/sec

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Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

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Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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	4	53.2	31.3	13377	6	US-10-311-455-1436	Sequence 1436, Ap

5	53.2	31.3	13377	7	US-10-221-714A-198	Sequence 198, App
6	52.4	30.8	16914	7	US-10-221-613-214	Sequence 214, App
7	50.6	29.8	10762	7	US-10-240-589C-131	Sequence 131, App
8	50.6	29.8	11691	6	US-10-311-455-2214	Sequence 2214, Ap
9	50.2	29.5	3673778	6	US-10-312-841-2	Sequence 2, Appli
c 10	50	29.4	385	7	US-10-424-599-86585	Sequence 86585, A
11	50	29.4	467	7	US-10-021-323-6541	Sequence 6541, Ap
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13	49.6	29.2	5867	7	US-10-433-793-181	Sequence 181, App
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c 16	49	28.8	539	8	US-10-425-115-172904	Sequence 172904,
17	49	28.8	2354	8	US-10-602-494-100	Sequence 100, App
18	49	28.8	2354	8	US-10-602-494-242	Sequence 242, App
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22	48.6	28.6	9106	6	US-10-240-452-70	Sequence 70, Appl
23	48.6	28.6	14006	6	US-10-311-455-1932	Sequence 1932, Ap
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33	47.4	27.9	9204	6	US-10-311-455-1101	Sequence 1101, Ap
34	47.4	27.9	9204	7	US-10-221-613-153	Sequence 153, App
c 35	47.2	27.8	277	3	US-09-960-352-12673	Sequence 12673, A
36	47.2	27.8	539	3	US-09-814-353-17862	Sequence 17862, A
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38	47	27.6	587	8	US-10-425-115-91618	Sequence 91618, A
39	47	27.6	6823	6	US-10-311-455-1117	Sequence 1117, Ap
40	47	27.6	7113	6	US-10-311-455-778	Sequence 778, App
41	47	27.6	12592	7	US-10-221-613-57	Sequence 57, Appl
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44	46.8	27.5	549	7	US-10-021-323-7101	Sequence 7101, Ap
45	46.8	27.5	6029	7	US-10-240-589C-65	Sequence 65, Appl

#### ALIGNMENTS

##### RESULT 1

US-09-883-343A-19

; Sequence 19, Application US/09883343A

; Publication No. US20030039632A1

##### GENERAL INFORMATION:

; APPLICANT: Stiles, Michael E.

; APPLICANT: Vederas, John C.

; APPLICANT: van Belkum, Marius J.

; APPLICANT: Worobo, Randy W.

; APPLICANT: Worobo, Rodney J.

; APPLICANT: Greer, G. Gordon

; APPLICANT: McMullen, Lynn M.

; APPLICANT: Leisner, Jorgen J.

; APPLICANT: Poon, Alston

; APPLICANT: Franz, Charles M.A.P.

; TITLE OF INVENTION: No. US20030039632A1elBacteriocins, Transport and Vector System and Metho

; FILE REFERENCE: 660.0005US

; CURRENT APPLICATION NUMBER: US/09/883,343A

; CURRENT FILING DATE: 2001-06-19

; PRIOR APPLICATION NUMBER: US/08/924,629

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; APPLICANT: Stiles, Michael E.
; APPLICANT: Vederas, John C.
; APPLICANT: van Belkum, Marius J.
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; APPLICANT: Worobo, Rodney J.
; APPLICANT: Greer, G. Gordon
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; TITLE OF INVENTION: No. US20030039632A1elBacteriocins, Transport and Vector System and Metho.
; FILE REFERENCE: 660.0005US
; CURRENT APPLICATION NUMBER: US/09/883,343A
; CURRENT FILING DATE: 2001-06-19
; PRIOR APPLICATION NUMBER: US/08/924,629
; PRIOR FILING DATE: 1997-09-05
; PRIOR APPLICATION NUMBER: US 60/026,257
; PRIOR FILING DATE: 1996-09-05
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# SCORE Search Results Details for Application 09883343 and Search Result us-09-883-343a- 19.rnpbn.

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# SUMMARIES

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# ALIGNMENTS

## RESULT 1

US-10-932-182A-166169/c

; Sequence 166169, Application US/10932182A

; Publication No. US20060046253A1

## GENERAL INFORMATION:

; APPLICANT: NAKAO, YOSHIHIRO

; APPLICANT: NAKAMURA, NORIHISA

; APPLICANT: KODAMA, YUKIKO

; APPLICANT: FUJIMURA, TOMOKO

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US-10-932-182A-166169/c
; Sequence 166169, Application US/10932182A
; Publication No. US20060046253A1
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; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: 030685-043
; CURRENT APPLICATION NUMBER: US/10/932,182A
; CURRENT FILING DATE: 2004-09-02
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# SCORE Search Results Details for Application 09883343 and Search Result us-09-883-343a-19.rni.

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OM nucleic - nucleic search, using sw model

Run on: May 3, 2006, 00:12:16 ; Search time 101 Seconds  
(without alignments)  
2991.935 Million cell updates/sec

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Sequence: 1 atgaaaataaaatggtactg.....tataaaaagataaacaata 170

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 1303057 seqs, 888780828 residues

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Post-processing: Minimum Match 0%  
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query		DB	ID	Description
		Match	Length			
1	170	100.0	170	3	US-08-924-629C-19	Sequence 19, Appl
2	170	100.0	3475	3	US-08-924-629C-15	Sequence 15, Appl
3	48.8	28.7	178883	3	US-09-949-016-12733	Sequence 12733, A
4	48.8	28.7	178884	3	US-09-949-016-13039	Sequence 13039, A
c 5	45	26.5	6250	3	US-09-724-857-4	Sequence 4, Appli

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c	34	41	24.1	8220	2	US-08-568-459A-11	Sequence 11, Appl
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c	36	41	24.1	8220	3	US-09-210-288-11	Sequence 11, Appl
c	37	41	24.1	8220	3	US-10-153-273-11	Sequence 11, Appl
c	38	41	24.1	19124	2	US-08-487-826B-13	Sequence 13, Appl
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	40	40.8	24.0	396	3	US-09-640-173-33	Sequence 33, Appl
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	42	40.8	24.0	396	3	US-09-825-294-33	Sequence 33, Appl
	43	40.8	24.0	396	3	US-09-970-966-33	Sequence 33, Appl
	44	40.8	24.0	19124	2	US-08-487-826B-13	Sequence 13, Appl
c	45	40.6	23.9	582	3	US-09-949-016-61868	Sequence 61868, A

#### ALIGNMENTS

#### RESULT 1

US-08-924-629C-19

; Sequence 19, Application US/08924629C

; Patent No. 6403082

#### ; GENERAL INFORMATION:

; APPLICANT: Stiles, Michael E.

; APPLICANT: Vederas, John C.

; APPLICANT: van Belkum, Marius J.

; APPLICANT: Worobo, Randy W.

; APPLICANT: Worobo, Rodney J.

; APPLICANT: Greer, G. Gordon

; APPLICANT: McMullen, Lynn M.

; APPLICANT: Leisner, Jorgen J.

; APPLICANT: Poon, Alston

; APPLICANT: Franz, Charles M.A.P.

; TITLE OF INVENTION: No. 6403082elBacteriocins, Transport and Vector System and Method of Use

; FILE REFERENCE: 660.0005US

; CURRENT APPLICATION NUMBER: US/08/924,629C

; CURRENT FILING DATE: 1997-09-05

; PRIOR APPLICATION NUMBER: US 60/026,257

; PRIOR FILING DATE: 1996-09-05



; NUMBER OF SEQ ID NOS: 80  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 19  
; LENGTH: 170  
; TYPE: DNA  
; ORGANISM: divergicin immunity gene;  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1)..(168)  
; OTHER INFORMATION:  
US-08-924-629C-19

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Matches 170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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## RESULT 2

US-08-924-629C-15

; Sequence 15, Application US/08924629C  
; Patent No. 6403082  
; GENERAL INFORMATION:

; APPLICANT: Stiles, Michael E.  
; APPLICANT: Vederas, John C.  
; APPLICANT: van Belkum, Marius J.  
; APPLICANT: Worobo, Randy W.  
; APPLICANT: Worobo, Rodney J.  
; APPLICANT: Greer, G. Gordon  
; APPLICANT: McMullen, Lynn M.  
; APPLICANT: Leisner, Jorgen J.  
; APPLICANT: Poon, Alston  
; APPLICANT: Franz, Charles M.A.P.

; TITLE OF INVENTION: No. 6403082elBacteriocins, Transport and Vector System and Method of Use  
; FILE REFERENCE: 660.0005US  
; CURRENT APPLICATION NUMBER: US/08/924,629C  
; CURRENT FILING DATE: 1997-09-05  
; PRIOR APPLICATION NUMBER: US 60/026,257  
; PRIOR FILING DATE: 1996-09-05  
; NUMBER OF SEQ ID NOS: 80  
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; LENGTH: 3475  
; TYPE: DNA  
; ORGANISM: plasmid;  
US-08-924-629C-15

Query Match 100.0%; Score 170; DB 3; Length 3475;  
Best Local Similarity 100.0%; Pred. No. 1.5e-24;  
Matches 170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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# SCORE Search Results Details for Application 09883343 and Search Result us-09-883-343a-19.rng.

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OM nucleic - nucleic search, using sw model

Run on: May 3, 2006, 22:29:58 ; Search time 305 Seconds  
(without alignments)  
3714.747 Million cell updates/sec

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Perfect score: 170  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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	2	170	100.0	170	2	AAX17722	Aax17722 Divergici
	3	170	100.0	3475	2	AAV11696	Aav11696 Plasmid p
	4	170	100.0	3475	2	AAX17720	Aax17720 Food-grad
c	5	56.4	33.2	416	8	ABX39419	Abx39419 Bovine ES
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	10	50.6	29.8	6118	6	ABN80110	Abn80110 Human che
	11	50.6	29.8	10762	6	ABL92322	Abl92322 Chemicall
	12	50.6	29.8	11691	6	ABL34241	Abl34241 Human imm
	13	50	29.4	467	13	ACN51760	Acn51760 Cotton an
c	14	49.6	29.2	531	13	ACN51594	Acn51594 Cotton an
	15	49.6	29.2	5867	6	ABQ67151	Abq67151 Human ang
	16	49.4	29.1	531	13	ACN51594	Acn51594 Cotton an
	17	49	28.8	2354	14	ADW10295	Adw10295 Colon pro
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c	19	48.8	28.7	469	13	ACN62049	Acn62049 Cotton gy
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	21	48.6	28.6	359	5	ADL43469	Adl43469 Human ova
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	28	47.8	28.1	608	5	ADL37588	Adl37588 Human ova
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	36	47.4	27.9	9204	6	AAS61194	Aas61194 Human gen
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	39	47.2	27.8	539	5	ADL43972	Adl43972 Human ova
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# ALIGNMENTS

## RESULT 1

AAV11698

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XX

AC AAV11698;

XX

DT 25-MAR-2003 (revised)

DT 14-SEP-1998 (first entry)

XX

DE Divergicin immunity gene.

XX

KW Divergicin; bacteriocin; signal peptide; protein secretion; preservative;

KW food spoilage; lactic acid bacterium; antibacterial; immunity gene; ss.

XX

OS Carnobacterium divergens.

XX

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ID      AAX17722 standard; DNA; 170 BP.
XX
AC      AAX17722;
XX
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# SCORE Search Results Details for Application 09883343 and Search Result us-09-883-343a-19.rge.

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OM nucleic - nucleic search, using sw model

Run on: May 3, 2006, 22:38:02 ; Search time 2068 Seconds  
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15: gb\_pl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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No.	Score	Match Length DB	ID			Description

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4	170	100.0	3475	6	AR212583	AR212583 Sequence
5	170	100.0	3475	6	BD006995	BD006995 Novel bac
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c 7	54.4	32.0	90347	5	AL714030	AL714030 Zebrafish
c 8	54.4	32.0	99681	5	AL713850	AL713850 Zebrafish
c 9	54.4	32.0	160905	5	BX571969	BX571969 Zebrafish
10	53.2	31.3	13377	6	AX251230	AX251230 Sequence
11	53.2	31.3	13377	6	AX346365	AX346365 Sequence
c 12	52.8	31.1	186250	13	AY380826	AY380826 Lymphocys
13	52.4	30.8	16914	6	AX251953	AX251953 Sequence
14	52.4	30.8	16914	6	AX348748	AX348748 Sequence
c 15	52.2	30.7	250029	2	AE014838	AE014838 Plasmodiu
c 16	52.2	30.7	252394	2	AE014833	AE014833 Plasmodiu
17	52	30.6	128352	15	AC144591	AC144591 Medicago
18	52	30.6	135950	14	CR848821	CR848821 Danio rer
19	51.8	30.5	4910	2	AF465313	AF465313 Dictyoste
20	51.8	30.5	39984	2	AC114258	AC114258 Dictyoste
c 21	51.8	30.5	257109	2	AC116963	AC116963 Dictyoste
c 22	51.6	30.4	251551	2	AE014844	AE014844 Plasmodiu
c 23	51.2	30.1	242710	14	AC138733	AC138733 Pongo pyg
24	51.2	30.1	331039	2	AC116979	AC116979 Dictyoste
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32	50.6	29.8	302156	2	AC116977	AC116977 Dictyoste
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37	49.8	29.3	286208	14	AC117140	AC117140 Rattus no
38	49.6	29.2	5867	6	AX458635	AX458635 Sequence
39	49.6	29.2	102344	14	AC141838	AC141838 Apis mell
40	49.6	29.2	110000	2	AC116305_2	Continuation (3 of
c 41	49.6	29.2	110435	14	CR956642	CR956642 Danio rer
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c 43	49.6	29.2	215018	14	AC139113	AC139113 Pongo pyg
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c 45	49.4	29.1	88549	2	AC116924	AC116924 Dictyoste

#### ALIGNMENTS

#### RESULT 1

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 DEFINITION Sequence 19 from patent US 6403082.  
 ACCESSION AR212585  
 VERSION AR212585.1 GI:23309309  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unknown.  
 Unclassified.  
 REFERENCE 1 (bases 1 to 170)  
 AUTHORS Stiles,M.E., Vederas,J.C., Van Belkum,M.J., Worobo,R.W.,  
 Worobo,R.J., McCormick,J.K., Greer,G.G., McMullen,L.M.,  
 Leisner,J.J., Poon,A. and Franz,C.M.A.P.  
 TITLE Bacteriocins, transport and vector system and method of use thereof

JOURNAL Patent: US 6403082-A 19 11-JUN-2002;

FEATURES Location/Qualifiers  
source 1. .170  
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ORIGIN

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RESULT 2

BD006997

LOCUS BD006997 170 bp DNA linear PAT 31-JAN-2002

DEFINITION Novel bacteriocins, transport and vector system and method of use thereof.

ACCESSION BD006997

VERSION BD006997.1 GI:18635368

KEYWORDS JP 2001503970-A/5.

SOURCE unidentified

ORGANISM unidentified

unclassified.

REFERENCE 1 (bases 1 to 170)

AUTHORS Stiles,M.E., Vederasu,J.C., Berukumu,M.J.V., Worobo,R.W.,  
Worobo,R.J., McCormick,J.K., Gordon,G.G., McMallen,L.M.,  
Reizuneru,J.J., Poone,A. and Frantz,C.M.A.P.

TITLE Novel bacteriocins, transport and vector system and method of use

JOURNAL Patent: JP 2001503970-A 5 27-MAR-2001;  
GOVERNORS OF THE UNIVERSITY OF ALBERTA

COMMENT OS Unidentified

PN JP 2001503970-A/5

PD 27-MAR-2001

PF 05-SEP-1997 JP 1998512914

PR 05-SEP-1996 US 60/026257

PI MICHAEL E STILES,JOHN C VEDERASU,MARIUS J VAN BERUKUMU, PI

RODNEY W WOROBO,

PI RODNEY J WOROBO,JOHN K MCCORMICK,GRIER G GORDON, PI LYNN M  
MCMALLEN,

PI JORGEN J REIZUNERU,ALISON POONE,CHARLES M A P FRANTZ PC

C12N15/09,A01K37/18,A23L1/30,A23L1/305,A61K38/00,A61P31/00, PC

A61P31/04,

PC C07K14/335,C07K16/12,C12N1/1/21,C12P21/02,C12P21/08,C12N15/00,

PC A61K37/02

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CC Topology: Linear;

FH Key Location/Qualifiers

FT CDS 1. .168.

FEATURES Location/Qualifiers

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/db\_xref="taxon:32644"

ORIGIN

# SCORE Search Results Details for Application 09883343 and Search Result us-09-883-343a-19.rst.

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OM nucleic - nucleic search, using sw model

Run on: May 3, 2006, 22:47:34 ; Search time 3721 Seconds  
(without alignments)  
2137.545 Million cell updates/sec

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Perfect score: 170  
Sequence: 1 atgaaaataaaatggtactg.....tataaaaagataaacaata 170

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

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Maximum Match 100%  
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6: gb\_est5:\*  
7: gb\_est6:\*  
8: gb\_est7:\*  
9: gb\_gss1:\*  
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11: gb\_gss3:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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c 3	55.2	32.5	168	1	AU074456	AU074456 AU074456	



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c	7	53	31.2	240	1	AU071622	AU071622 AU071622
	8	53	31.2	1201	10	CNS0167M	AL106396 Drosophil
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	11	52.4	30.8	978	8	DN563011	DN563011 87653490
	12	52.2	30.7	927	9	AZ046250	AZ046250 nbab0091D
	13	51.6	30.4	530	5	BX566754	BX566754 BX566754
c	14	51.6	30.4	600	8	DN351463	DN351463 LIB3579-0
	15	51.4	30.2	1200	10	CNS0162Z	AL106229 Drosophil
c	16	51.2	30.1	187	1	AU071758	AU071758 AU071758
	17	51.2	30.1	926	3	BM394635	BM394635 50072-2-5
	18	51.2	30.1	970	10	CNS0182E	AL108800 Drosophil
	19	51.2	30.1	1023	8	DN568261	DN568261 90172339
	20	51	30.0	240	1	AU072475	AU072475 AU072475
c	21	51	30.0	540	7	CO885816	CO885816 BovGen_14
	22	51	30.0	947	10	CZ524990	CZ524990 GMW2-62N1
c	23	51	30.0	986	8	DN575739	DN575739 90182439
c	24	50.6	29.8	340	8	DN863041	DN863041 nab40d08.
c	25	50.6	29.8	1044	10	CNS005D6	AL058139 Drosophil
c	26	50.6	29.8	1101	10	CNS003DX	AL064587 Drosophil
c	27	50.4	29.6	767	10	CNS00AQX	AL055924 Drosophil
	28	50.4	29.6	999	10	CW942426	CW942426 TcB23.4_G
c	29	50.4	29.6	1092	10	CNS020K7	AL175696 Tetraodon
c	30	50.4	29.6	1101	10	CNS00Z2U	AL097152 Drosophil
c	31	50.2	29.5	858	5	BU935417	BU935417 AGENCOURT
	32	50.2	29.5	1100	9	BZ696700	BZ696700 SP_Ba008
c	33	50.2	29.5	1383	10	CL510075	CL510075 SAIL_823_
c	34	50	29.4	313	5	BQ391420	BQ391420 NISC_mq18
c	35	49.8	29.3	506	8	DN353227	DN353227 LIB3580-0
	36	49.8	29.3	644	7	CV226785	CV226785 WS0165.B2
	37	49.8	29.3	1008	8	DN563433	DN563433 92240038
c	38	49.8	29.3	1101	10	CNS00ZBM	AL097468 Drosophil
	39	49.8	29.3	1160	8	DR732342	DR732342 FGAS07826
	40	49.6	29.2	709	8	DN137796	DN137796 ACAE-aaa0
	41	49.6	29.2	761	8	CX585478	CX585478 TTE000268
c	42	49.6	29.2	905	10	CNS00KHX	AL077798 Drosophil
c	43	49.4	29.1	162	2	BI268723	BI268723 NF023E03G
	44	49.4	29.1	230	5	BX473837	BX473837 DKFZp686H
	45	49.4	29.1	230	8	DN892016	DN892016 naol7g08.

# ALIGNMENTS

## RESULT 1

DN572350/c

LOCUS DN572350 1004 bp mRNA linear EST 14-MAR-2005

DEFINITION 92239480 Sea Urchin primary mesenchyme cell cDNA library  
Strongylocentrotus purpuratus cDNA clone PMCSRP2-166A11 3', mRNA  
sequence.

ACCESSION DN572350

VERSION DN572350.1 GI:61131389

KEYWORDS EST.

SOURCE Strongylocentrotus purpuratus

ORGANISM Strongylocentrotus purpuratus

Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;  
Echinoidea; Euechinoidea; Echinacea; Echinoidea;  
Strongylocentrotidae; Strongylocentrotus.

REFERENCE 1 (bases 1 to 1004)

AUTHORS Zhu,X., Mahairas,G., Illies,M.R., Cameron,R.A., Davidson,E.H. and  
Ettensohn,C.A.

TITLE A large scale analysis of mRNAs expressed by primary mesenchyme  
cells of the sea urchin embryo

JOURNAL	Development 128 (13), 2615-2627 (2001)
PUBMED	11493577
COMMENT	Contact: Erica Sodergren Human Genome Sequencing Center Baylor College of Medicine One Baylor Plaza, Houston, TX 77030, USA Tel: 713-798-7676 Fax: 713-798-6977 Email: ericas@bcm.tmc.edu NCBI Trace Archive: 486722151 Insert Length: 1750 Std Error: 0.25 Plate: 166 row: A column: 11.

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FEATURES             Location/Qualifiers
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                        /organism="Strongylocentrotus purpuratus"
                        /mol_type="mRNA"
                        /db_xref="taxon:7668"
                        /clone="PMCSRP2-166A11"
                        /tissue_type="embryo"
                        /cell_type="primary mesenchyme cells"
                        /lab_host="E.coli"
                        ./clone_lib="Sea Urchin primary mesenchyme cell cDNA
                        library"
                        /note="Vector: pSPORT1; Site_1: NotI; Site_2: MluI; oligo
                        dt priming from poly A+ RNA, directionally cloned"

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## ORIGIN

Query Match 34.9%; Score 59.4; DB 8; Length 1004;  
Best Local Similarity 60.0%; Pred. No. 0.65;  
Matches 99; Conservative 0; Mismatches 66; Indels 0; Gaps 0;

Qy	5	AAATAAAATGGTACTGGGAATCTCTGATTGAAACCTTAATATTTATAATTGTTCTTCTTG	64
Db	521	AATTAAAAGGGAATTTTAATTTTAAATTTACAAAATTAAAATTAAAATTTTTTTTTTTTTT	462
Qy	65	TATTTTTTTTATAGAAGTCTCGGTTTTTCTTTAAAAAATTTAGTTTTAGGAAGTTTATTTT	124
Db	461	TTTTTTTTTAAAAAAATTTTATTTTTTTTTTAAACCCTTTTTTTTTTAAAAATTTTTTTA	402
Qy	125	ATTTGATAGCAATTGGTCTTTTTTAATTATAAAAAGATAAACAAAT	169
Db	401	AAAAAAATTATCTTTTTTTTTTACACTAAATTAAAAAAAAAAAAAAT	357

## RESULT 2

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CNS00AIS/c
LOCUS      CNS00AIS              783 bp    DNA        linear    GSS 03-JUN-1999
DEFINITION Drosophila melanogaster genome survey sequence TET3 end of BAC #
            BACR21G10 of RPCI-98 library from Drosophila melanogaster (fruit
            fly), genomic survey sequence.
ACCESSION  AL055833
VERSION    AL055833.1  GI:4936400
KEYWORDS   GSS.
SOURCE     Drosophila melanogaster (fruit fly)
  ORGANISM Drosophila melanogaster
            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
            Ephydroidea; Drosophilidae; Drosophila.
REFERENCE  1 (bases 1 to 783)
  AUTHORS  Genoscope.
  TITLE    Direct Submission
  JOURNAL  Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
            BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
            - Web : www.genoscope.cns.fr)
COMMENT    Determination of this BAC-end sequence was carried out as part of a
            collaboration with the Berkeley Drosophila Genome Project (BDGP).
```